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Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank

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Abstract

Depression is more frequent among individuals exposed to traumatic events. Both trauma exposure and depression are heritable. However, the relationship between these traits, including the role of genetic risk factors, is complex and poorly understood. When modelling trauma exposure as an environmental influence on depression, both gene-environment correlations and gene-environment interactions have been observed. The UK Biobank concurrently assessed Major Depressive Disorder (MDD) and self-reported lifetime exposure to traumatic events in 126,522 genotyped individuals of European ancestry. We contrasted genetic influences on MDD between individuals reporting and not reporting trauma exposure (final sample size range: 24,094-92,957). The SNP-based heritability of MDD was greater in participants reporting trauma exposure (24%) than in individuals not reporting trauma exposure (12%), taking into account the strong, positive genetic correlation observed between MDD and reported trauma exposure. The genetic correlation between MDD and waist circumference was only significant in individuals reporting trauma exposure ($r_g = 0.24$, $p = 1.8 \times 10^{-7}$ versus $r_g = -0.05$, $p = 0.39$ in individuals not reporting trauma exposure, difference $p = 2.3 \times 10^{-4}$). Our results suggest that the genetic contribution to MDD is greater when additional risk factors are present, and that a complex relationship exists between reported trauma exposure, body composition, and MDD.

1 **Introduction**

2 Depression is among the most common mental illnesses worldwide and
3 accounts for 5.5% of all years lost through disability globally ¹. In England
4 approximately 28% of individuals self-report depression during their lifetime ². The
5 most common clinically recognised form of depression is called Major Depressive
6 Disorder (MDD). Both environmental and genetic factors influence MDD. In
7 particular, MDD is more commonly observed among individuals reporting exposure
8 to stressful life events and early-life traumas ³⁻⁶. In turn, reported trauma exposure
9 has been robustly correlated with a range of adverse life outcomes including MDD ⁶⁻
10 ⁹. The relationship between MDD and reported trauma exposure is complex, with
11 studies showing both that reported trauma exposure is associated with subsequent
12 MDD, and that MDD is associated with subsequent reported trauma exposure ^{10,11}.
13 However, the majority of people reporting exposure to traumatic experiences do not
14 report MDD ⁶⁻⁹.

15 Twin studies show that MDD is moderately heritable, with 30-40% of the
16 variance in MDD attributable to genetic factors ¹². The proportion of heritability
17 captured by common genetic variants, also known as single nucleotide
18 polymorphism or **SNP-based** heritability, can be estimated from genome-wide
19 association study (GWAS) data. Such estimates tend to be lower than those
20 obtained from twin approaches, due to the incomplete capture of genetic information
21 in GWAS data among other reasons ¹³. The most recent major depression GWAS
22 from the Psychiatric Genomics Consortium was anchored in 35 cohorts (including
23 the 23andMe discovery cohort ¹⁴) recruited with a variety of methods ¹⁵. This meta-
24 analysis identified 44 loci significantly associated with major depression, and
25 estimated a **SNP-based** heritability of 9-10% ¹⁵. GWAS results strongly suggest both

1 the mild and more severe forms of depression are polygenic, with potentially
2 thousands of variants with very small individual effects contributing to risk.

3 There are far fewer genetic studies of reported trauma exposure than of MDD.
4 However, the available studies have demonstrated that reported trauma exposure is
5 heritable, with twin heritability estimates of 20-50% ¹⁶⁻¹⁸ and **SNP-based** heritability
6 estimates of 30% ¹⁹. Combining measures of trauma exposure and depression on a
7 large scale is difficult and, as with many environmental measures, requires careful
8 phenotyping ²⁰. Potential confounds include the (often unavoidable) use of
9 retrospective self-reported measures of trauma exposure, which can be weakly
10 correlated with objective measures of traumatic experiences ⁹. Furthermore, current
11 (i.e. state) low mood or MDD can increase self-reporting of previous trauma
12 exposure ^{9,21}. Previous individual study cohorts have generally been too small for
13 effective GWAS, while meta-analyses have contained considerable heterogeneity
14 due to the use of different phenotyping instruments in the included studies.

15 However, some notable genome-wide analyses of MDD and trauma exposure
16 have been performed. A genome-wide by environment interaction study of
17 depressive symptoms and stressful life events in 7,179 African American women
18 identified a genome-wide association near the *CEP350* gene (although this did not
19 replicate in a smaller cohort) ²². A recent investigation in 9,599 Han Chinese women
20 with severe MDD identified three variants associated with MDD specifically in
21 individuals who did not report exposure to traumatic events prior to MDD onset ²³.

22 Several attempts have been made to estimate the interaction of overall
23 genetic risk and trauma by using polygenic risk scores for MDD to perform **polygenic**
24 **risk score**-by-trauma interaction analyses. Such studies test whether there are
25 departures from additivity (where the combined effect of **risk score** and trauma differs

1 from the sum of the individual effects) or from multiplicativity (where the combined
2 effect differs from the product of the individual effects). Results from these have
3 been highly **variable**, with reports of significant additive and multiplicative interactions
4 ²⁴; significant multiplicative interactions only ²⁵; and, in the largest previous study
5 published (a meta-analysis of 5,765 individuals), no interactions ²⁶.

6 **Studies of gene-environment interaction usually assume the genetic and**
7 **environmental influences are independent and uncorrelated ²⁷. However, genetic**
8 **correlations between reported trauma exposure and MDD have been reported, both**
9 **from twin studies ^{28–30} and from the genomic literature ^{22,26}. Reports of the magnitude**
10 **of this genetic correlation have varied widely, which reflects differences in defining**
11 **trauma exposure, and in the populations studied. While some studies have identified**
12 **a very high genetic correlation (95%) ²², others have found no such correlation ²³.**
13 **The relationship between reported trauma exposure and MDD, and the influence of**
14 **genetic variation on that relationship, is therefore complex and unresolved.**

15 The release of mental health questionnaire data from the UK Biobank
16 resource provides an opportunity to assess the relationship between genetic
17 variation, risk for MDD, and reported trauma exposure in a single large cohort. We
18 performed GWAS of probable MDD with and without reported lifetime trauma
19 exposure in UK Biobank European ancestry individuals. **These GWAS were**
20 **underpowered to detect individual genetic loci at the very low effect sizes seen in**
21 **previous GWAS of MDD. However, these results enabled us to estimate the SNP-**
22 **based** heritability of MDD in individuals with and without reported lifetime trauma
23 exposure, **and so to test whether the relative contribution of genetic influences to**
24 **MDD differs in the context of reported trauma exposure.** We then estimated the
25 genetic correlation between MDD in the two groups, **to assess whether the genetic**

component differed between individuals reporting and not reporting trauma exposure. In addition, we compared the patterns of genetic correlation between MDD in these groups and a wide range of physical and psychiatric traits, in order to assess whether the genetic relationship of MDD to other traits varies in the context of reported trauma exposure. Finally, we performed polygenic risk scoring, using external traits commonly comorbid with MDD, and sought to extend previous analyses of PRS-by-trauma interactions in MDD.

Methods

Phenotype definitions

The UK Biobank assessed a range of health-related phenotypes and biological measures including genome-wide genotype data in approximately 500,000 British individuals aged between 40 and 70³¹. This includes 157,366 participants who completed an online follow-up questionnaire assessing common mental health disorders, including MDD symptoms, and 16 items assessing traumatic events (Resource 22 on <http://biobank.ctsu.ox.ac.uk>)³². Phenotypes were derived from this questionnaire, using definitions from a recent publication describing its phenotypic structure³².

Individuals with probable MDD met lifetime criteria based on their responses to questions derived from the Composite International Diagnostic Interview (CIDI; Supplementary Table 1). We excluded cases if they self-reported previous diagnoses of schizophrenia, other psychoses, or bipolar disorder. Controls were excluded if they self-reported any mental illness, reported taking any drug with an antidepressant indication, had previously been hospitalised with a mood disorder or met previously-defined criteria for a mood disorder (Supplementary Table 1)³³.

1 Participants were asked questions relating to traumatic experiences in
2 childhood using the Childhood Trauma Screener (a shortened version of the
3 Childhood Trauma Questionnaire ^{34–36}) and an equivalent screener for adulthood
4 developed by the UK Biobank Mental Health steering group to mirror the childhood
5 items ³². In addition, participants were asked questions related to events that
6 commonly trigger post-traumatic stress-disorder (PTSD). Responses to individual
7 questions (items) in these three categories (child trauma, adult trauma, PTSD-
8 relevant trauma) were dichotomised and compared between MDD cases and
9 controls (Supplementary Table 2a).

10 We selected reported items with an odds ratio > 2.5 with MDD, to obtain a
11 single binary variable for stratification that captured exposure to the traumatic events
12 most associated with MDD. Items from all three trauma categories were reported
13 more in MDD cases compared to controls. Of the selected items, three referred to
14 events in childhood (did not feel loved, felt hated by a family member, sexually
15 abused). Another three items referred to events in adulthood (physical violence,
16 belittlement, sexual interference), and one item assessed a PTSD-relevant event
17 (ever a victim of sexual assault). In order to capture increased severity of exposure,
18 only individuals reporting two or more of these items were included as reporting
19 trauma exposure. Individuals reporting none of the items were included as not
20 reporting trauma exposure. Individuals reporting a single trauma item, or who did not
21 provide an answer were excluded from the analyses (Supplementary Table 1). A
22 breakdown of reported traumatic experiences by sex and MDD status is provided in
23 Supplementary Table 2b. Further discussion of the definition of trauma exposure is
24 included in the Supplementary Note.

25

1 Phenotype preparation for analyses

2 Three sets of analyses comparing MDD cases and controls were performed
3 (i) overall, (ii) limited to individuals reporting trauma exposure, and (iii) limited to
4 individuals not reporting trauma exposure (Table 1). In addition, sensitivity analyses
5 were performed on reported trauma exposure (overall and stratified by MDD
6 diagnosis; see Supplementary Methods and Results, and Supplementary Table 3).
7 For each analysis, phenotypes were first residualised on 6 ancestry principal
8 components from the genetic data of the European samples as well as factors
9 capturing initial assessment centre and genotyping batch. More details on phenotype
10 preparation can be found in the Supplementary Methods.

11

12 Phenotype distribution

13 Previous analyses have shown that, compared to the participants in the UK
14 Biobank as a whole, those who completed the mental health questionnaire were
15 more likely to have a university degree, came from a higher socioeconomic
16 background, and reported fewer long-standing illnesses or disabilities³².
17 Accordingly, participants were compared across a number of standard demographic
18 variables and common correlates of MDD: sex, age (at questionnaire), education
19 (university degree vs. not), neighbourhood socioeconomic status (SES, as
20 Townsend deprivation index³⁷) and BMI (recorded from measurements taken at the
21 initial recruitment of the participants into the biobank). For further details on these
22 analyses, see Supplementary Methods.

1 Genetic data

2 Genetic data for GWAS analyses came from the full release of the UK
3 Biobank data (N=487,410; ³⁸). Autosomal genotype data from two highly-overlapping
4 custom genotyping arrays (covering ~800,000 markers) underwent centralised
5 quality control before being imputed in a two-stage imputation to the Haplotype
6 Reference Consortium (HRC) and UK10K (for rarer variants not present in the HRC)
7 reference panels ³⁸⁻⁴⁰. In addition to this central quality control, variants for analysis
8 were limited to common variants (minor allele frequency > 0.01) that were either
9 directly genotyped or imputed from the HRC with high confidence (IMPUTE INFO
10 metric > 0.4) ³⁹.

11 Individuals were excluded where recommended by the UK Biobank core
12 analysis team for unusual levels of missingness or heterozygosity, or if they had
13 withdrawn consent for analysis. Using the genotyped SNPs, individuals with call rate
14 < 98%, who were related to another individual in the dataset (KING $r < 0.044$,
15 equivalent to removing up third-degree relatives and closer ⁴¹) or whose phenotypic
16 and genotypic gender information was discordant (X-chromosome homozygosity (F_X)
17 < 0.9 for phenotypic males, $F_X > 0.5$ for phenotypic females) were also excluded.
18 Removal of relatives was performed using a "greedy" algorithm, which minimises
19 exclusions (for example, by excluding the child in a mother-father-child trio). All
20 analyses were limited to individuals of European ancestry, as defined by 4-means
21 clustering on the first two genetic principal components provided by the UK Biobank
22 ⁴². This ancestry group included 95% of the respondents to the mental health
23 questionnaire - as such, the non-European ancestry groups were considered too
24 small to analyse informatively. Principal components analysis was also performed on
25 the European-only subset of the data using the software flashpca2 ⁴³. After quality

control, individuals with high-quality genotype data and who had completed the online mental health questionnaire were retained for analysis (N=126,522). GWAS analyses used the imputed data as described above. Genetic correlation analyses used the results of the GWAS analyses. Polygenic risk score analyses and SNP-based heritability analyses in BOLT-LMM used the genotyped variants³⁸. These latter analyses were limited to common variants (minor allele frequency > 0.01) with call rate >98% that were in approximate Hardy-Weinberg equilibrium (HWE test $p > 10^{-8}$). The same individuals were used for analyses using the imputed and the genotyped data.

Analyses

Genome Wide Association Studies (GWAS)

GWAS were performed to assess the association of individual genetic variants with MDD. These analyses were first undertaken for the entire sample regardless of reported trauma exposure, then stratified by reported trauma exposure. GWAS were performed using linear regressions on imputed genotype dosages in BGenie v1.2³⁸, with residualised phenotypes as described above. Phenotypes and genotypes were mean-centred and standardised. Genome-wide significance was defined at the conventional level $p < 5 \times 10^{-8}$ ⁴⁴. Results from each GWAS were clumped to define genetic loci in PLINK2⁴⁵. Loci were defined following established protocols (Supplementary Methods)¹⁵.

Betas from the GWAS were converted to odds ratios (OR) using LMOR (<http://cnsgenomics.com/shiny/LMOR/>) and observed sample prevalences⁴⁶. Standard errors were calculated from the p-value and estimated OR⁴⁷. Performing GWAS on residuals, rather than including covariates in the analysis, is a restriction

1 imposed by the BGenie software (which was used because it is specifically designed
2 for analysing the UK Biobank genetic data). Sensitivity analyses were performed to
3 test for biases resulting from this method. Specifically, for each GWAS, each variant
4 with nominal significance ($p < 0.0001$) was also tested using logistic regression
5 including covariates in R 3.4.1, in order to confirm the results from BGenie ⁴⁸.

6

7 **SNP-based heritability**

8 Results from GWAS were combined to assess the proportion of variance due
9 to the additive effect of common genetic variants (SNP-based heritability). SNP-
10 based heritability was calculated on the observed scale using BOLT-LMM v2.3 ⁴⁹.
11 The estimate for MDD in the cohort was converted to the liability scale in R 3.4.1,
12 assuming a population prevalence of 28% ^{2,50}. Converting estimates of SNP-based
13 heritability for a case-control trait from the observed scale to the liability scale
14 requires accurate estimates of the lifetime prevalence of the trait in the
15 (sub)population. When comparing a trait stratified by a correlated variable (as is the
16 case when we compare the SNP-based heritability of MDD stratified by reported
17 trauma exposure), the population prevalence in each stratum is unknown. To
18 address this, we approximated the expected prevalence of MDD in individuals either
19 reporting or not reporting trauma exposure (Supplementary Methods). This allowed
20 us to convert the observed scale SNP-based heritability of MDD to the liability scale
21 in both strata (i.e. those reporting and those not reporting trauma exposure). A
22 second challenge is that trauma exposure is itself a heritable trait that is genetically
23 correlated with MDD in this study. The potential impact of this on SNP-based
24 heritability estimation is not intuitive. To benchmark our findings, we performed
25 simulations of SNP-level data to explore the expected SNP-based heritability of MDD

1 in individuals reporting and not reporting trauma exposure, assuming differences in
2 **SNP-based** heritability resulted only from the genetic correlation between MDD and
3 reported trauma exposure. Further details of these analyses are provided in the
4 Supplementary Methods.

6 **Genetic correlations**

7 Genetic correlations (r_g) were calculated to assess shared genetic influences
8 between MDD and other phenotypes, using GWAS summary statistics and LD Score
9 regression v1.0.0⁵¹ using the default HapMap LD reference. Two sets of genetic
10 correlations were calculated. First, we calculated genetic correlations between the
11 phenotypes examined within this paper (internal phenotypes). We calculated the
12 genetic correlation between MDD and reported trauma exposure in the full dataset,
13 and then the genetic correlation between MDD in individuals reporting trauma
14 exposure and MDD in individuals not reporting trauma exposure. Secondly, we also
15 calculated genetic correlations between each GWAS from this analysis and a
16 curated list of 308 publicly-available phenotypes (external phenotypes)^{51,52}.

17 Genetic correlations were tested for difference from 0 (default in LD Score),
18 and for difference from 1 (in Microsoft Excel, converting r_g to a chi-square as $[(r_g - 1)/se]^2$)^{51,52}. Genetic correlations were considered significant if they passed the
19 Bonferroni-adjusted threshold for the effective number of traits studied in each
20 analysis (internal: $p < 0.01$; external: $p < 2.5 \times 10^{-4}$). The effective number of traits was
21 calculated as the number of principal components explaining 99.5% of the variance
22 in the pairwise genetic correlation matrix (internal: 5; external: 202). External
23 phenotype GWAS all had heritability estimates such that $h^2/SE > 2$, and produced
24 valid (i.e. non-NA) r_g with all other phenotypes tested.

1 The genetic correlation of MDD with each external phenotype was compared
2 between individuals reporting trauma exposure and individuals not reporting trauma
3 exposure using a two-stage method. First, differences were assessed using two
4 sample z-tests⁵³. Nominally-significant differences ($p < 0.05$) by this method were
5 then compared using the block-jackknife (Supplementary Methods)^{52,54,55}. Results
6 using the jackknife were considered significant if they passed the Bonferroni-
7 adjusted threshold ($p < 2.5 \times 10^{-4}$).

9 Polygenic Risk Scoring

10 Polygenic risk scores were calculated to further assess shared genetic
11 influences between MDD and traits known to be correlated to MDD. Specifically, risk
12 scores from analyses of major depression (MDD)¹⁵, schizophrenia (SCZ)⁵⁶, bipolar
13 disorder (BIP)⁵⁷, body mass index (BMI)⁵⁸ and glycated haemoglobin (HbA1c; used
14 as a negative control)⁵⁹ were calculated and compared in all participants and
15 stratifying by reported trauma exposure. The PGC major depression GWAS
16 contained participants from UK Biobank, so to derive the MDD risk score we used a
17 restricted set of summary statistics without these individuals (but including
18 individuals from 23andMe, whose diagnoses were self-reported¹⁴). For further
19 discussion of this overlap, see Supplementary Note¹⁵. Risk scores were calculated
20 using PRSice v2 (<https://github.com/choishingwan/PRSice>^{45,60}) at seven thresholds
21 (external GWAS $p < 0.001, 0.05, 0.1, 0.2, 0.3, 0.4$ and 0.5) to allow assessment of
22 the spread of association between risk score and MDD. Analyses used logistic
23 regression, including all covariates used in creating the residuals for GWAS. In total,
24 five external phenotypes were used to produce risk scores for the three target
25 phenotypes (MDD overall, and stratified by reported trauma exposure/non-

1 exposure), resulting in 15 analyses. A conservative Bonferroni adjustment for
2 multiple testing was used, correcting for 105 tests (seven thresholds and 15
3 analyses), giving a final threshold for significance of $p < 0.0004$.

4 In addition to these stratified analyses, we performed formal risk score-by-
5 environment analyses to estimate the effect on MDD of the interaction between
6 genetic variants across the whole genome (modelled as a risk score) and reported
7 trauma exposure. We calculated interactions between reported trauma exposure and
8 the risk score capturing the most variance from each of the main-effect polygenic risk
9 score analyses. These analyses included the same covariates used in the GWAS,
10 and all risk score-by-covariate and reported trauma exposure-by-covariate
11 interactions^{61,62}. Both multiplicative and additive interactions were tested. A
12 significant multiplicative interaction means that the combined effect of the risk score
13 and reported trauma exposure differs from the product of their individual effects.
14 Multiplicative interactions were tested using logistic regression^{25,26}. A significant
15 additive interaction means that the combined effect of the risk score and reported
16 trauma exposure differs from the sum of their individual effects. Additive interactions
17 were tested using linear regression (Supplementary Methods).

19 Sensitivity analyses

20 Differences in phenotypic variables were observed between cases and
21 controls. To assess the impact of including these variables as covariates, all
22 analyses were rerun retaining all previous covariates and including as further
23 covariates: age (at questionnaire), neighbourhood socioeconomic status (SES, as
24 Townsend deprivation index³⁷), BMI (at baseline assessment), and a binary variable
25 of education (university degree vs. not). The same covariates were also included in

polygenic risk score and SNP-based heritability analyses. Sensitivity analyses focussing on reported trauma exposure as an outcome were similarly rerun (Supplementary Methods).

The majority of the sample with data on both MDD symptoms and reported trauma status were controls who did not report trauma (Table 1). To assess whether this disbalance in sample status affected our results, genetic correlation analyses with external phenotypes were rerun on ten downsampled cohorts, each with 9,487 participants (the number of cases not reporting trauma exposure; see Supplementary Methods).

In order to test whether our definition of trauma exposure affected the main finding of our paper, we performed three further sensitivity analyses, redefining reported trauma exposure. First, we assessed if our main finding was robust to changing the threshold for including MDD-relevant trauma, by redefining reported trauma exposure as a report of i) one or more and ii) three or more of the seven MDD-relevant trauma items. Second, we assessed whether the timing of trauma exposure affected this finding by redefining reported trauma exposure as a report of iii) one or more of the five childhood trauma items. We then re-analysed the heritability of MDD in individuals reporting and not reporting trauma exposure using these three alternative definitions.

Results

Phenotype distribution

Phenotypic and genetic data were available on 24,094 to 92,957 individuals (Table 1). Overall, 36% of individuals met our definition of MDD-relevant trauma exposure, and were more frequently cases (45%) than controls (17%; OR = 5.23; $p <$

1 10^{-50} , chi-square test). We assessed a number of phenotypic correlates of
2 depression to confirm that these correlates differed between MDD cases and
3 controls, and to assess whether these differences were affected by trauma
4 exposure. Cases differed significantly from controls overall. Individuals with MDD
5 were mostly females, significantly younger, less likely to have a university degree,
6 came from more deprived neighbourhoods, and had higher BMI at recruitment.
7 These differences persisted when the cohort was limited just to individuals reporting
8 trauma exposure, and when the cohort was limited just to individuals not reporting
9 trauma exposure. Furthermore, cases reporting trauma exposure differed from cases
10 not reporting trauma exposure, in that they were mostly females, younger, more
11 likely to have a degree (note difference from case-control comparisons), came from
12 more deprived neighbourhoods, and had higher BMI at recruitment. The same
13 differences (in the same direction) were observed between controls reporting and not
14 reporting trauma exposure (all $p < 0.05$; Supplementary Table 4).

		Participants with genomic data			
		Reported trauma exposure	No reported trauma exposure	Excluded	Total
MDD	Cases	13,393^b	9,487^c	6,595	29,475^a
	Controls	10,701^b	39,677^c	13,104	63,482^a

Table 1: Participants available for analysis.

Groups of individuals used in each of the three analyses are in bold.

The superscripts denote the groups used in each of the three main analyses:

a) MDD in all participants (29,475 cases, 63,482 controls, $N = 92,957$);

b) MDD in participants reporting trauma exposure
(13,393 cases, 10,701 controls, $N = 24,094$);

c) MDD in participants not reporting trauma exposure
(9,487 cases, 39,677 controls, $N = 49,164$).

1 Genome-wide association studies

2 We performed GWAS for MDD overall and stratified by reported trauma
3 exposure to obtain results for heritability and genetic correlation analyses
4 (Supplementary Table 6; Supplementary Figures 1-3). No analysis showed evidence
5 of genome-wide inflation that was attributable to confounding (95% confidence
6 intervals of all regression intercepts from LD Score included 1; Supplementary Table
7 7). One genome-wide significant locus (rs11515172, Chr 9:11Mb, $p = 3.82 \times 10^{-8}$) was
8 identified in the analysis of MDD overall, and remained significant when using logistic
9 regression ($p = 4.69 \times 10^{-8}$, OR = 0.96, SE = 0.007; Supplementary Table 6). This
10 locus has been repeatedly associated with depression^{15,63,64} and with neuroticism^{65–}
11⁶⁸; however, it should be noted that all of these studies included UK Biobank. The
12 locus is intergenic, and is not annotated to any currently known biological feature of
13 interest (Supplementary Table 8).

14

15 SNP-based heritability

16 First we estimated the observed scale SNP-based heritability of MDD overall
17 and stratified by reported trauma exposure. Second, in order to assess whether the
18 relative influence of genetic variants on MDD differed by reported trauma status, we
19 converted SNP-heritabilities to the liability scale. We assumed a prevalence of 28%
20 for self-reported MDD in the full population². Based on this, and on the ratio of MDD
21 cases:controls in the sample, we estimated the prevalence of MDD in the trauma-
22 exposed population as 52%, and in the unexposed population as 17%. Using these
23 estimates of population prevalence, the liability scale estimate of MDD SNP-based
24 heritability was 20% (95% confidence interval: [18-22%]) overall. In those reporting
25 trauma exposure, the liability scale SNP-based heritability of MDD was 24% [18-

31%], and in those not reporting trauma exposure it was 12% [7-16%]. The SNP-based heritability of MDD was significantly greater in individuals who reported trauma exposure compared to those who did not ($p = 0.0021$, Z-test).

These estimated SNP-heritabilities could be confounded by genetic correlation between MDD and reported trauma exposure. We conducted simulations of SNP-level data to quantify the expected difference in SNP-based heritability from genetic correlation alone. Our simulations yielded expected estimates for the liability scale SNP-based heritability of MDD of 14-15% in those reporting trauma exposure, and 15-16% in those not reporting trauma exposure (Supplementary Methods). This small difference in expected SNP-based heritability for those reporting and not reporting trauma is in the opposite direction to our findings. This suggests that our findings cannot be explained by genetic correlation between MDD and reported trauma exposure, nor by the transformation from the observed scale to the liability scale.

Genetic correlations

Genetic correlations were calculated between MDD and reported trauma to explore the genetic relationship between these traits. Further genetic correlations were calculated between MDD in the two strata to assess whether genetics influences on MDD differ in the context of reported trauma exposure (Supplementary Table 10).

We observed a significant r_g between MDD and reported trauma exposure in the full cohort (0.62 [95% CI: 0.76-0.94], $p < 10^{-50}$). Given that trauma items were selected for association with MDD, we also calculated the genetic correlation between MDD in the full cohort and reported trauma exposure in just the controls,

1 which was also significantly greater than 0 (0.31 [0.18-0.45], $p = 4 \times 10^{-6}$;
2 Supplementary Table 10). This correlation persisted when using independent major
3 depression GWAS summary statistics, as reported trauma exposure was
4 significantly correlated with the MDD polygenic risk score (Spearman's $\rho = 0.0675$,
5 $p < 10^{-50}$)¹⁵. The genetic correlation between MDD in individuals reporting trauma
6 exposure and MDD in individuals not reporting trauma exposure was high and did
7 not differ significantly from 1 ($r_g = 0.77$ [0.48-1.05]; difference from 0: $p = 1.8 \times 10^{-7}$;
8 difference from 1: $p = 0.11$).

9 Genetic correlations were calculated between MDD and all available external
10 traits to systematically assess whether genetic relationships with MDD differed in the
11 context of reported trauma exposure. All psychiatric traits included were significantly
12 associated ($p < 2.5 \times 10^{-4}$) with MDD, but this association did not differ substantially in
13 magnitude between the groups reporting and not reporting trauma exposure (z-test
14 for comparisons of $r_g - \Delta r_g$ - ranged from $p = 0.10 - 0.99$; Figure 1). In contrast, waist
15 circumference was significantly associated with MDD only in individuals reporting
16 trauma exposure ($r_g = 0.24$), and the correlation was significantly larger than that in
17 individuals not reporting trauma exposure ($r_g = -0.05$, jackknife $p_{\Delta r_g} = 2.3 \times 10^{-4}$). Other
18 correlations between MDD and body composition, reproductive, and socioeconomic
19 phenotypes were larger in the group reporting trauma exposure compared to
20 individuals not reporting trauma exposure, but these differences did not remain
21 significant following multiple testing correction (all jackknife $p > 2.5 \times 10^{-4}$; Figure 1,
22 Supplementary Table 11).

Polygenic risk scores across strata

We performed polygenic risk score analyses to further explore how stratification by trauma status affects the genetic relationship between MDD and specific correlates of MDD, and to mirror previous analyses in the literature (Figure 2, Table 2; see Supplementary Table 12 for full details of all risk score analyses, including the number of SNPs in each score)²⁶. Individuals with high genetic risk scores for MDD were more likely to be cases than controls, and a significant additive interaction term was observed from linear regression. Specifically, the combined effect of the MDD risk score and reported trauma exposure on MDD was greater than the sum of the individual effects ($\beta > 0$, Table 2 central panel). However, the multiplicative interaction term was not significant ($p > 0.01$). The presence of an interaction on the additive scale reflects the greater SNP-based heritability of MDD in individuals reporting trauma exposure ($\text{SNP-}h^2 = 24\%$) compared to those not reporting trauma exposure ($\text{SNP-}h^2 = 12\%$), as described above.

In contrast, although those with higher BMI risk scores were more likely to be cases than controls, this only passed correction for multiple testing in individuals reporting trauma exposure. Both the additive ($\beta > 0$) and the multiplicative ($\text{OR} > 0$) interaction terms were significant, suggesting the combined effect on MDD from BMI risk score and reported trauma exposure together was greater than expected from both the sum of the individual risks and from their product, respectively ($\text{OR} > 1$).

Individuals with high genetic risk scores for SCZ were more likely to be cases than controls, but this did not differ between strata (both interaction terms $p > 0.01$). Individuals with higher BIP risk scores were also more likely to be cases than controls - although this association was not significant in the subset of individuals

- 1 reporting trauma exposure, no significant interaction term was observed, suggesting
- 2 the observed difference in results within-strata may be due to differences in power.
- 3 No significant differences were observed in the negative control analysis with HbA1c.

Base	Base N	Best Threshold	Analysis	PRS			PRS x Reported Trauma					
				OR	95% CI	p	Additive			Multiplicative		
							Beta	95% CI	p	OR	95% CI	p
MDD	116,404 // 314,990	0.5	<i>MDD</i>	1.26	1.24-1.28	< 10⁻⁵⁰	0.011	0.008-0.014	2.69x10⁻¹¹	1.01	1.00 - 1.03	0.132
SCZ	36,989 // 113,075	0.3		1.11	1.09-1.12	1.11 x 10⁻⁴¹	0.008	-0.003-0.004	0.659	0.99	0.97-1.00	0.158
BIP	7,481 // 9,250	0.2		1.07	1.05-1.08	4.57 x 10⁻¹⁹	-0.000	-0.003-0.003	0.961	0.99	0.97-1.00	0.165
BMI	339,224	0.3		1.04	1.03-1.06	2.60 x 10⁻⁸	0.006	0.003-0.009	1.13x10⁻⁴	1.02	1.01-1.04	0.0074
HB1Ac	46,368	0.001		1.01	1.00-1.02	0.163	0.002	-0.001-0.005	0.186	1.01	0.99-1.02	0.391
MDD	116,404 // 314,990	0.4	<i>MDD, reported trauma exposure</i>	1.24	1.21-1.27	< 10⁻⁵⁰						
SCZ	36,989 // 113,075	0.5		1.06	1.03-1.09	2.96 x 10⁻⁵						
BIP	7,481 // 9,250	0.5		1.04	1.01-1.07	0.00329						
BMI	339,224	0.5		1.07	1.04-1.10	1.85 x 10⁻⁷						
HB1Ac	46,368	0.001		1.02	1.00-1.05	0.0863						
MDD	116,404 // 314,990	0.4	<i>MDD, no reported trauma exposure</i>	1.21	1.18-1.23	< 10⁻⁵⁰						
SCZ	36,989 // 113,075	0.5		1.09	1.06-1.11	4.34 x 10⁻¹²						
BIP	7,481 // 9,250	0.2		1.07	1.04-1.09	4.05 x 10⁻⁸						
BMI	339,224	0.3		1.02	1.00-1.04	0.0980						
HB1Ac	46,368	0.001		1.01	0.99-1.03	0.492						

Table 2: Main effect and interaction effects for polygenic risk scores (PRS) associated with MDD overall and in stratified analyses. Interaction effects are on the **additive scale (Beta)** and the **multiplicative scale (OR)**. Bold = significant associations (main analyses: $p < 0.000143$; interactions: $p < 0.01$). Base N = Cases // Controls. OR/Beta = Increase with 1 SD increase in **risk score** or trauma exposure. Results are reported at the "best" threshold (that with the lowest p-value in main effect analyses) - results across all thresholds are reported in Supplementary Table 12.

1 Sensitivity analyses

2 Four sets of sensitivity analyses were performed. In the first set, all analyses
3 were repeated using reported trauma exposure as the phenotype, assessed overall
4 and stratified by MDD (as opposed to the primary analysis, where MDD was the
5 phenotype and analyses were stratified by reported trauma exposure). Results from
6 these analyses were broadly similar to the results from the primary analysis
7 (Supplementary Tables 3-12, Supplementary Figures 4-7).

8 The second set of sensitivity analyses repeated the primary analyses with
9 additional covariates to assess the impact of controlling for age, neighbourhood
10 socioeconomic status, BMI, and education. This did not alter the conclusions drawn
11 from the GWAS and SNP-based heritability analyses, nor from the genetic
12 correlations observed between the internal phenotypes (those assessed in this
13 study; Supplementary Tables 13-18). Genetic correlations between MDD and
14 external phenotypes did not differ significantly from the main analysis (all z-test $p <$
15 0.05), but were sufficiently attenuated that the genetic correlations of MDD with waist
16 circumference was no longer significantly different between individuals reporting and
17 not reporting trauma exposure. Differences in the polygenic risk score analyses were
18 limited to analyses involving the BMI risk score. The BMI risk score was no longer
19 associated with MDD in any analysis, and no interactions including the BMI risk
20 score remained significant. This suggests the effects of the BMI risk score in the
21 main analysis likely result from BMI differences between MDD cases and controls,
22 rather than being true effects on MDD.

23 The third set of sensitivity analyses repeated the genetic correlation analyses,
24 but downsampled the analysed cohort such that each of the four groups (MDD
25 cases/controls reporting/not reporting trauma exposure) had 9,487 participants (the

size of the smallest group from the main analysis, cases not reporting trauma exposure). In these analyses, genetic correlations between MDD and external phenotypes were attenuated across most phenotypes, but not significantly (two-sample z-tests, all $p > 0.05$; Supplementary Table 19). As such, the general pattern of genetic correlations observed in the main analysis was retained, although the genetic correlations of MDD with waist circumference was no longer significantly different between individuals reporting and not reporting trauma exposure.

The final set of sensitivity analyses repeated the SNP-based heritability analyses of MDD in individuals reporting and not reporting trauma exposure, altering the definition of reported trauma exposure in three ways (increasing and decreasing the number of items required to be defined as reporting trauma exposure, and limiting the items considered to only childhood experiences). The purpose of these analyses was to test the robustness of our key finding (greater MDD SNP-based heritability in trauma-exposed individuals compared to those not reporting trauma exposure). Neither increasing nor decreasing the number of MDD-relevant items selected, nor focussing on childhood items, altered our conclusions (Supplementary Table 20).

Full results for all four sensitivity analyses are included in the Supplementary Material.

Discussion

We investigated the relationship between MDD and self-reported trauma exposure in the largest single cohort available to date (N=73,258 with MDD and reported trauma data). We examined individual genetic variants, SNP-based heritability, genetic correlations, and polygenic risk scores. The SNP-based

1 heritability of MDD was higher in individuals reporting trauma exposure than in
2 individuals not reporting trauma exposure. This was not attributable to gene-
3 environment correlation, nor to the transformation of SNP-based heritability from the
4 observed to the liability scale. Despite the significant difference in SNP-based
5 heritability across the two strata, the genetic correlation between MDD in individuals
6 reporting and not reporting trauma exposure was not statistically different from 1.
7 Polygenic risk score-by-reported trauma exposure interaction analyses identified
8 significant interactions for both MDD and BMI risk scores. However, the interactions
9 involving the BMI risk score appear to reflect differences in measured BMI between
10 MDD cases and controls, rather than differences directly related to MDD. Finally, a
11 significant genetic correlation between MDD and waist circumference was observed
12 only in individuals reporting trauma exposure, and was absent from those not
13 reporting trauma exposure.

14

15 A number of limitations should be considered when assessing our results. Our
16 simulations suggest that the significantly higher SNP-based heritability of MDD in
17 individuals reporting trauma exposure did not result from gene-environment
18 correlation between MDD and reported trauma exposure, nor from the
19 transformation of the observed scale SNP-based heritability to the liability scale.
20 However, we could not address further sources of potential bias. These could arise
21 from genetic architectures other than those simulated (including non-additive genetic
22 effects), from intrinsic challenges of heritability estimation in case-control data
23 (including ascertainment bias and the effects of covariates not included in the model)
24 ^{69,70}, or from potential collider bias (the induction of a correlation between two
25 uncorrelated variables by conditioning on a third unknown variable correlated with

1 both) resulting from selection bias ⁷¹. We also assumed that the population
2 prevalence of reported trauma exposure can be extrapolated from that observed in
3 this sample (see Supplementary Methods). Although the UK Biobank allows us to
4 integrate genetic and environmental data at scale, and is a reasonably
5 homogeneous cohort, it also has a "healthy volunteer bias", whereby the participants
6 tend to have better overall health and higher socioeconomic status compared to the
7 equivalent overall population of this age ⁷². It is possible that the depressive and
8 traumatic experiences reported by these participants may not generalise to the
9 whole population, or to clinically-ascertained cases. Furthermore, we focussed on
10 European ancestry; further studies in non-European populations are required ⁷³.

11 To obtain further insight into the association of genome-wide genetic variation
12 and reported trauma exposure with MDD (and to enable comparison with previous
13 studies ^{24–26}), we carried out polygenic risk score-by-environment interaction
14 analyses. There are a number of limitations to consider when interpreting such
15 analyses. Polygenic risk score-by-environment interaction analyses test a specific
16 hypothesis, namely that the overall association of common variants with the outcome
17 (modelled as a risk score) varies dependent on the environmental exposure being
18 tested. As such, the absence of an interaction does not preclude the existence of
19 specific variant-by-environment interactions, including those featuring variants
20 contributing to the risk score. Furthermore, we cannot exclude the possibility that the
21 correlation between the MDD risk score and reported trauma exposure may alter the
22 observed interaction. As such, caution is needed before drawing strong conclusions,
23 especially given the small effect sizes, and limited predictive power, of risk scores in
24 this study (Supplementary Table 12).

1 Throughout this paper, we have referred to our depression phenotype as
2 "MDD" rather than "major depression". We do this because our definition is based on
3 the CIDI-SF, which has previously been shown to have good concordance with direct
4 clinical assessments of MDD ^{74,75}. However, it should be noted that direct
5 assessment was not performed, and our probable MDD cases may not have met
6 criteria within a clinical setting. Nonetheless, genetic correlations between studies of
7 MDD and of major depression are high, suggesting there is strong genetic continuity
8 across different methods of assessing depression ^{15,64}.

9 Trauma exposure was defined in this study using retrospective self-report.
10 This is not the ideal measure for this phenotype, and precludes robust measurement
11 of the severity and timing of the reported trauma exposure. However, retrospective
12 report is the only feasible option in large cohorts like the UK Biobank. The
13 requirement for cohort sizes large enough to identify the small individual genetic
14 effects typical of complex genetic traits such as MDD makes self-report the most
15 practicable method of data-collection. Retrospectively reported trauma and MDD
16 data are not robust to reverse causation, and our results cannot strongly inform any
17 temporal or causal hypotheses about the relationship between trauma and MDD.
18 Such hypotheses could be tested using longitudinal studies (with the inherent
19 logistical difficulties in obtaining both environmental and genomic data) or through
20 more powerful genomic studies of trauma exposure in a larger cohort. This latter
21 design would enable the identification of sufficient robustly associated genetic
22 variants to inform approaches such as Mendelian randomisation (which we were
23 underpowered to examine in this study). In addition, future work may benefit from
24 assessing the heritability of broader depression phenotypes that lie beyond our
25 binary criteria, including reward sensitivity and negative valence traits ⁷⁶.

1
2 Our findings suggest that the genetic variants associated with MDD are the
3 same in individuals reporting and not reporting trauma exposure, because the
4 genetic correlation between MDD measured in these two groups was not
5 significantly different from 1. However, the SNP-based heritability of MDD was
6 *greater* in individuals reporting compared to not reporting trauma exposure. This
7 suggests that the combined effect of the variants associated with MDD is greater in
8 people reporting trauma exposure than in those who do not. The mechanism
9 underlying this finding is uncertain. One possibility is that exposure to traumatic
10 events might amplify genetic influences on MDD beyond the magnitude of the effects
11 seen in the absence of trauma (consistent with the stress-diathesis hypothesis ^{77–79}).
12 The concept that genetic variance varies with exposure to different environments is
13 well-recognised in studies of animal populations in the wild ⁸⁰. However, the opposite
14 may also be true; genetic influences on MDD could increase an individual's likelihood
15 of experiencing and/or reporting of trauma, and through doing so increase the
16 apparent heritability of MDD by partly incorporating genetic influences related to
17 trauma reporting itself ¹¹. A final possibility relates to the components of variance
18 involved in calculating SNP-based heritability. Phenotypic variance can be attributed
19 either to the SNPs measured in the GWAS, or to environmental sources of variance
20 reflecting all phenotypic variance not explained by common variants. It is possible
21 that the genetic component of variance is constant across the strata, but that the
22 environmental component is smaller in individuals reporting trauma exposure, for
23 example due to the shared (and thus more similar/less variable) exposure of these
24 individuals to MDD-relevant traumatic experiences. This would result in greater
25 heritability in individuals reporting trauma exposure. We provide these explanations

1 as potential interpretations of these findings. However, these are not the only
2 possibilities, and it is also likely that multiple such mechanisms are involved.

3
4 In polygenic risk score-by-reported trauma exposure interaction analyses, we
5 identified a significant interaction on the additive scale for the combined effect of the
6 MDD risk score and reported trauma exposure on risk of MDD. These results are
7 also reflected in the larger SNP-based heritability of MDD in exposed compared to
8 unexposed individuals. The simplest explanation for this result is that the effects of
9 the MDD risk score and reported trauma exposure on MDD combine multiplicatively,
10 such that their combined effects are greater than the sum of their individual effects.
11 For the BMI risk score however, the interaction with reported trauma exposure
12 appears to be more complex, combining neither additively nor multiplicatively. In
13 sensitivity analyses controlling for BMI (obtained at recruitment, approximately five
14 years before the mental health questionnaire), the BMI risk score-by-reported trauma
15 exposure interaction was no longer significant, suggesting that the observed
16 interaction can be explained by differences in measured BMI. Further research, with
17 concurrent measurements of BMI, trauma exposure and MDD in a longitudinally-
18 sampled cohort would offer further insight into the relationship between these three
19 variables.

20 The high genetic correlation between MDD in individuals reporting and not
21 reporting trauma exposure was supported by significant genetic correlations between
22 MDD and other psychiatric disorders regardless of reported trauma exposure. In
23 individuals reporting trauma exposure, a further significant genetic correlation was
24 observed between MDD and waist circumference, which was significantly greater
25 than the equivalent correlation in those not reporting trauma exposure. Although not

1 significant, there was also a general pattern of higher genetic correlations between
2 MDD and several weight-related measures and educational attainment, in individuals
3 reporting trauma exposure. This is consistent with previous literature on traumatic
4 experiences across the life course, and related phenomena such as Adverse
5 Childhood Experiences (ACEs). This literature has found that such adversities are
6 associated not only with psychiatric risk but also with wide-ranging impairments in
7 social and health outcomes including obesity and education ^{81–84}. However, we
8 stress that causal conclusions cannot be drawn from these data, or that the reported
9 trauma exposure is responsible for the observed differences.

10 Our estimate of the SNP-based heritability of MDD (20%) is higher than that
11 reported in previous studies of major depression (~9%) ¹⁵. This may be explained by
12 the relative homogeneity of the UK Biobank compared to previous meta-analyses.
13 The UK Biobank is a single-country cohort ascertained using a consistent protocol.
14 The same questionnaire was used to gather symptom data, and the samples were
15 stored, extracted, and genotyped using a single method. In contrast, meta-analyses
16 have needed to combine diverse ascertainment, sampling, and genotyping; SNP-
17 based heritability has been reported to decrease with increasing numbers of meta-
18 analysed samples ⁸⁵. Previous analyses have assessed alternative depression
19 phenotypes in the UK Biobank ⁶⁴. Our MDD phenotype (based on DSM criteria for
20 MDD) is most similar to the probable MDD phenotype from Howard et al, rather than
21 the less strictly-defined "broad depression" phenotype, which includes those who
22 seek treatment for depression, anxiety and related phenotypes. More specifically the
23 "broad depression" phenotypes includes many people with MDD, but also many
24 people who may not meet diagnostic criteria for MDD or instead have anxiety
25 disorders or a similar closely related common mental disorder. Our MDD phenotype

1 includes only those people who meet diagnostic criteria (using the CIDI
2 questionnaire). Our estimate from BOLT-LMM (19.9%) is within the bounds of the
3 reported range of GREML estimates by geographic region reported for the probable
4 MDD (0% to 27.5%) phenotype. Our LDSC-based estimate is higher than the
5 equivalent from Howard et al (4-5%). However, the estimate from Howard et al is
6 considerably lower than previous estimates ¹⁵, and potentially lacks both the
7 specificity of definitions from clinical practice or structured questionnaires, and the
8 sensitivity of broad phenotyping methods.

9 Our results also differ in several respects from those of a study of MDD and
10 adversity in Han Chinese women ²³. No difference in the SNP-based heritability of
11 MDD between individuals reporting and not reporting trauma exposure was observed
12 in the previous study, and we did not replicate individual variant results. However,
13 this is unsurprising, as there are a number of differences between the studies of
14 which the primary one is sample size (this study: 73,258; CONVERGE: 9,599). Other
15 differences included culture and ethnicity, and the deeper phenotyping methodology
16 applied in CONVERGE, resulting in a severe inpatient MDD phenotype. Notably, the
17 previous study did not report a genetic correlation between MDD and trauma
18 exposure ²³.

19 Sensitivity analyses focussed on trauma found that self-reported traumatic
20 experience was significantly heritable, as has been previously observed ¹⁹. We
21 strongly emphasise that this does not necessarily imply that traumatic experiences
22 themselves have a biological component - such experiences may be associated with
23 other significantly heritable traits, and their biology would then be reflected in the
24 observed heritability of trauma exposure. One potential set of heritable traits that
25 may be associated with reporting traumatic experiences are personality traits such

1 as risk-taking, and this might explain the observed genetic correlations with
2 psychiatric traits. A similar phenomenon has been proposed to underlie observed
3 genetic correlations with socioeconomic status⁸⁶. Our trauma exposure measure
4 relies on retrospective self-report, which is itself correlated with personality traits and
5 mood at time of report⁹. This may also explain the genetic correlations we observe
6 with reported trauma exposure (including in controls, who do not report previous
7 psychiatric illness).

8
9 In summary, we find that genetic associations with MDD in UK Biobank vary
10 by context. Specifically, the SNP-based heritability of MDD is larger in individuals
11 reporting trauma exposure compared to those not doing so. Furthermore, the genetic
12 correlation of MDD with waist circumference was significant only in individuals
13 reporting exposure to trauma. Nonetheless, a strong genetic correlation was
14 observed between MDD measured in the two strata. Together, these findings
15 suggest the relative contribution of genetic variants to variance in MDD is greater
16 when additional risk factors are present.

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12

13 **Figure legends**

14 **Figure 1:** Genetic correlations between MDD (overall and stratified by reported
15 trauma exposure) and selected traits and disorders. Full genetic correlation results
16 are available in Supplementary Table 11. Numbers = genetic correlations. Colour =
17 direction of effect (blue = positive, red = negative). Colour intensity = size of
18 correlation. Upper and lower bars are 95% confidence interval of genetic correlation.

19

20 **Figure 2:** Association between MDD polygenic risk score (PRS) and MDD.
21 Individuals reporting trauma exposure are shown as orange triangles, and those not
22 reporting trauma exposure as green dots. Panel a shows the relationship on the
23 linear additive scale, and panel b shows the relationship on the multiplicative scale.
24 A significant interaction is observed on the additive scale only, as shown by differing
25 slopes of the two regression lines in panel a.

26

References

- 1 GBD 2016 Disease and Injury Incidence and Prevalence Collaborators. Global, regional, and national incidence, prevalence, and years lived with disability for 328 diseases and injuries for 195 countries, 1990-2016: a systematic analysis for the Global Burden of Disease Study 2016. *Lancet* 2017; **390**: 1211–1259.
- 2 McManus S, Bebbington P, Jenkins R, Brugha T. *Mental Health and Wellbeing in England: Adult Psychiatric Morbidity Survey 2014: a Survey Carried Out for NHS Digital by NatCen Social Research and the Department of Health Sciences, University of Leicester*. NHS Digital, 2016.
- 3 Green JG, McLaughlin KA, Berglund PA, Gruber MJ, Sampson NA, Zaslavsky AM *et al*. Childhood adversities and adult psychiatric disorders in the national comorbidity survey replication I: associations with first onset of DSM-IV disorders. *Arch Gen Psychiatry* 2010; **67**: 113–123.
- 4 Nanni V, Uher R, Danese A. Childhood maltreatment predicts unfavorable course of illness and treatment outcome in depression: a meta-analysis. *Am J Psychiatry* 2012; **169**: 141–151.
- 5 Kessler RC. The effects of stressful life events on depression. *Annu Rev Psychol* 1997; **48**: 191–214.
- 6 McLaughlin KA, Conron KJ, Koenen KC, Gilman SE. Childhood adversity, adult stressful life events, and risk of past-year psychiatric disorder: a test of the stress sensitization hypothesis in a population-based sample of adults. *Psychol Med* 2010; **40**: 1647–1658.
- 7 Kessler RC, Davis CG, Kendler KS. Childhood adversity and adult psychiatric disorder in the US National Comorbidity Survey. *Psychol Med* 1997; **27**: 1101–1119.
- 8 Collishaw S, Pickles A, Messer J, Rutter M, Shearer C, Maughan B. Resilience to adult psychopathology following childhood maltreatment: evidence from a community sample. *Child Abuse Negl* 2007; **31**: 211–229.
- 9 Baldwin JR, Reuben A, Newbury JB, Danese A. Agreement Between Prospective and Retrospective Measures of Childhood Maltreatment: A Systematic Review and Meta-analysis. *JAMA Psychiatry* 2019. doi:10.1001/jamapsychiatry.2019.0097.
- 10 Kendler KS, Karkowski LM, Prescott CA. Causal relationship between stressful life events and the onset of major depression. *Am J Psychiatry* 1999; **156**: 837–841.
- 11 Kendler KS, Karkowski-Shuman L. Stressful life events and genetic liability to major depression: genetic control of exposure to the environment? *Psychol Med* 1997; **27**: 539–547.

- 12 Polderman TJC, Benyamin B, de Leeuw CA, Sullivan PF, van Bochoven A, Visscher PM *et al.* Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nat Genet* 2015; **47**: 702–709.
- 13 Yang J, Zeng J, Goddard ME, Wray NR, Visscher PM. Concepts, estimation and interpretation of SNP heritability. *Nat Genet* 2017; **49**: 1304–1310.
- 14 Hyde CL, Nagle MW, Tian C, Chen X, Paciga SA, Wendland JR *et al.* Identification of 15 genetic loci associated with risk of major depression in individuals of European descent. *Nat Genet* 2016; **48**: 1031–1036.
- 15 Wray NR, Ripke S, Mattheisen M, Trzaskowski M, Byrne EM, Abdellaoui A *et al.* Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nat Genet* 2018; **50**: 668–681.
- 16 Jang KL, Vernon PA, Livesley WJ, Stein MB, Wolf H. Intra- and extra-familial influences on alcohol and drug misuse: a twin study of gene-environment correlation. *Addiction* 2001; **96**: 1307–1318.
- 17 Stein MB, Jang KL, Taylor S, Vernon PA, Livesley WJ. Genetic and environmental influences on trauma exposure and posttraumatic stress disorder symptoms: a twin study. *Am J Psychiatry* 2002; **159**: 1675–1681.
- 18 Lyons MJ, Goldberg J, Eisen SA, True W, Tsuang MT, Meyer JM *et al.* Do genes influence exposure to trauma? A twin study of combat. *Am J Med Genet* 1993; **48**: 22–27.
- 19 Power RA, Wingenbach T, Cohen-Woods S, Uher R, Ng MY, Butler AW *et al.* Estimating the heritability of reporting stressful life events captured by common genetic variants. *Psychol Med* 2013; **43**: 1965–1971.
- 20 Dunn EC, Brown RC, Dai Y, Rosand J, Nugent NR, Amstadter AB *et al.* Genetic determinants of depression: recent findings and future directions. *Harv Rev Psychiatry* 2015; **23**: 1–18.
- 21 Schraedley PK, Turner RJ, Gotlib IH. Stability of retrospective reports in depression: traumatic events, past depressive episodes, and parental psychopathology. *J Health Soc Behav* 2002; **43**: 307–316.
- 22 Dunn EC, Wiste A, Radmanesh F, Almli LM, Gogarten SM, Sofer T *et al.* GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. *Depress Anxiety* 2016; **33**: 265–280.
- 23 Peterson RE, Cai N, Dahl AW, Bigdeli TB, Edwards AC, Webb BT *et al.* Molecular Genetic Analysis Subdivided by Adversity Exposure Suggests Etiologic Heterogeneity in Major Depression. *Am J Psychiatry* 2018; **175**: 545–554.

- 24 Peyrot WJ, Milaneschi Y, Abdellaoui A, Sullivan PF, Hottenga JJ, Boomsma DI *et al.* Effect of polygenic risk scores on depression in childhood trauma. *Br J Psychiatry* 2014; **205**: 113–119.
- 25 Mullins N, Power RA, Fisher HL, Hanscombe KB, Euesden J, Iniesta R *et al.* Polygenic interactions with environmental adversity in the aetiology of major depressive disorder. *Psychol Med* 2016; **46**: 759–770.
- 26 Peyrot WJ, Van der Auwera S, Milaneschi Y, Dolan CV, Madden PAF, Sullivan PF *et al.* Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. *Biol Psychiatry* 2017. doi:10.1016/j.biopsych.2017.09.009.
- 27 Jaffee SR, Price TS. Gene-environment correlations: a review of the evidence and implications for prevention of mental illness. *Mol Psychiatry* 2007; **12**: 432–442.
- 28 Lau JYF, Eley TC. Disentangling gene-environment correlations and interactions on adolescent depressive symptoms. *J Child Psychol Psychiatry* 2008; **49**: 142–150.
- 29 Thapar A, Harold G, McGuffin P. Life events and depressive symptoms in childhood—shared genes or shared adversity? A research note. *J Child Psychol Psychiatry* 1998; **39**: 1153–1158.
- 30 Boardman JD, Alexander KB, Stallings MC. Stressful life events and depression among adolescent twin pairs. *Biodemography Soc Biol* 2011; **57**: 53–66.
- 31 Allen NE, Sudlow C, Peakman T, Collins R, UK Biobank. UK biobank data: come and get it. *Sci Transl Med* 2014; **6**: 224ed4.
- 32 Davis KAS, Coleman JRI, Adams M, Allen N, Breen G, Cullen B *et al.* Mental health in UK Biobank: development, implementation and results from an online questionnaire completed by 157 366 participants. *BJPsych Open* 2018; **4**: 83–90.
- 33 Smith DJ, Nicholl BI, Cullen B, Martin D, Ul-Haq Z, Evans J *et al.* Prevalence and characteristics of probable major depression and bipolar disorder within UK biobank: cross-sectional study of 172,751 participants. *PLoS One* 2013; **8**: e75362.
- 34 Bellis MA, Hughes K, Leckenby N, Perkins C, Lowey H. National household survey of adverse childhood experiences and their relationship with resilience to health-harming behaviors in England. *BMC Med* 2014; **12**: 72.
- 35 Bernstein DP, Fink L, Handelsman L, Foote J, Lovejoy M, Wenzel K *et al.* Initial reliability and validity of a new retrospective measure of child abuse and neglect. *Am J Psychiatry* 1994; **151**: 1132–1136.

- 36 Grabe HJ, Schulz A, Schmidt CO, Appel K, Driessen M, Wingenfeld K *et al.* [A brief instrument for the assessment of childhood abuse and neglect: the childhood trauma screener (CTS)]. *Psychiatr Prax* 2012; **39**: 109–115.
- 37 Townsend P, Phillimore P, Beattie A. *Health and Deprivation: Inequality and the North*. Croom Helm, 1988.
- 38 Bycroft C, Freeman C, Petkova D, Band G, Elliott LT, Sharp K *et al.* The UK Biobank resource with deep phenotyping and genomic data. *Nature* 2018; **562**: 203–209.
- 39 McCarthy S, Das S, Kretschmar W, Delaneau O, Wood AR, Teumer A *et al.* A reference panel of 64,976 haplotypes for genotype imputation. *Nat Genet* 2016; **48**: 1279–1283.
- 40 UK10K Consortium, Walter K, Min JL, Huang J, Crooks L, Memari Y *et al.* The UK10K project identifies rare variants in health and disease. *Nature* 2015; **526**: 82–90.
- 41 Manichaikul A, Mychaleckyj JC, Rich SS, Daly K, Sale M, Chen W-M. Robust relationship inference in genome-wide association studies. *Bioinformatics* 2010; **26**: 2867–2873.
- 42 Warren HR, Evangelou E, Cabrera CP, Gao H, Ren M, Mifsud B *et al.* Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nat Genet* 2017; **49**: 403–415.
- 43 Abraham G, Qiu Y, Inouye M. FlashPCA2: principal component analysis of Biobank-scale genotype datasets. *Bioinformatics* 2017; **33**: 2776–2778.
- 44 Dudbridge F, Gusnanto A. Estimation of significance thresholds for genomewide association scans. *Genet Epidemiol* 2008; **32**: 227–234.
- 45 Chang CC, Chow CC, Tellier LC, Vattikuti S, Purcell SM, Lee JJ. Second-generation PLINK: rising to the challenge of larger and richer datasets. *Gigascience* 2015; **4**: 7.
- 46 Lloyd-Jones LR, Robinson MR, Yang J, Visscher PM. Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. *Genetics* 2018. doi:10.1534/genetics.117.300360.
- 47 Marioni RE, Harris SE, Zhang Q, McRae AF, Hagenaars SP, Hill WD *et al.* GWAS on family history of Alzheimer's disease. *Transl Psychiatry* 2018; **8**: 99.
- 48 Team RC. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing; 2014. 2014.
- 49 Loh P-R, Kichaev G, Gazal S, Schoech AP, Price AL. Mixed-model association for biobank-scale datasets. *Nat Genet* 2018; **50**: 906–908.

- 50 Lee SH, Goddard ME, Wray NR, Visscher PM. A better coefficient of determination for genetic profile analysis. *Genet Epidemiol* 2012; **36**: 214–224.
- 51 Bulik-Sullivan BK, Loh P-R, Finucane HK, Ripke S, Yang J, Schizophrenia Working Group of the Psychiatric Genomics Consortium *et al.* LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. *Nat Genet* 2015; **47**: 291–295.
- 52 Bulik-Sullivan B, Finucane HK, Anttila V, Gusev A, Day FR, Loh P-R *et al.* An atlas of genetic correlations across human diseases and traits. *Nat Genet* 2015; **47**: 1236–1241.
- 53 Daniel. *Biostatistics: A Foundation For Analysis In Health Sciences, 7Th Ed.* Wiley India Pvt. Limited, 2006.
- 54 Tukey WJ. Bias and confidence in not-quite large samples. *Ann Math Stat* 1958; **29**: 614.
- 55 Quenouille MH. Notes on Bias in Estimation. *Biometrika* 1956; **43**: 353–360.
- 56 Schizophrenia Working Group of the Psychiatric Genomics Consortium. Biological insights from 108 schizophrenia-associated genetic loci. *Nature* 2014; **511**: 421–427.
- 57 Psychiatric GWAS Consortium Bipolar Disorder Working Group. Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. *Nat Genet* 2011; **43**: 977–983.
- 58 Locke AE, Kahali B, Berndt SI, Justice AE, Pers TH, Day FR *et al.* Genetic studies of body mass index yield new insights for obesity biology. *Nature* 2015; **518**: 197–206.
- 59 Soranzo N, Sanna S, Wheeler E, Gieger C, Radke D, Dupuis J *et al.* Common variants at 10 genomic loci influence hemoglobin A_{1c} levels via glycemic and nonglycemic pathways. *Diabetes* 2010; **59**: 3229–3239.
- 60 Euesden J, Lewis CM, O'Reilly PF. PRSice: Polygenic Risk Score software. *Bioinformatics* 2015; **31**: 1466–1468.
- 61 Keller MC. Gene × environment interaction studies have not properly controlled for potential confounders: the problem and the (simple) solution. *Biol Psychiatry* 2014; **75**: 18–24.
- 62 Yzerbyt VY, Muller D, Judd CM. Adjusting researchers' approach to adjustment: On the use of covariates when testing interactions. *J Exp Soc Psychol* 2004; **40**: 424–431.
- 63 Turley P, Walters RK, Maghzian O, Okbay A, Lee JJ, Fontana MA *et al.* Multi-trait analysis of genome-wide association summary statistics using MTAG. *Nat Genet* 2018; : 118810.

- 64 Howard DM, Adams MJ, Shirali M, Clarke T-K, Marioni RE, Davies G *et al.* Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. *Nat Commun* 2018; **9**: 1470.
- 65 Smith DJ, Escott-Price V, Davies G, Bailey MES, Colodro-Conde L, Ward J *et al.* Genome-wide analysis of over 106 000 individuals identifies 9 neuroticism-associated loci. *Mol Psychiatry* 2016; **21**: 749–757.
- 66 Luciano M, Hagenaars SP, Davies G, Hill WD, Clarke T-K, Shirali M *et al.* Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. *Nat Genet* 2018; **50**: 6–11.
- 67 Okbay A, Baselmans BML, De Neve J-E, Turley P, Nivard MG, Fontana MA *et al.* Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nat Genet* 2016; **48**: 624–633.
- 68 Nagel M, Jansen PR, Stringer S, Watanabe K, de Leeuw CA, Bryois J *et al.* Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways. *Nat Genet* 2018; **50**: 920–927.
- 69 Weissbrod O, Flint J, Rosset S. Estimating SNP Heritability and Genetic Correlation in Case-Control Studies Directly and with Summary Statistics. *Am J Hum Genet* 2018; **103**: 89–99.
- 70 Golan D, Lander ES, Rosset S. Measuring missing heritability: inferring the contribution of common variants. *Proc Natl Acad Sci U S A* 2014; **111**: E5272–81.
- 71 Munafò MR, Tilling K, Taylor AE, Evans DM, Davey Smith G. Collider scope: when selection bias can substantially influence observed associations. *Int J Epidemiol* 2018; **47**: 226–235.
- 72 Fry A, Littlejohns TJ, Sudlow C, Doherty N, Allen NE. OP41 The representativeness of the UK Biobank cohort on a range of sociodemographic, physical, lifestyle and health-related characteristics. *J Epidemiol Community Health* 2016; **70**: A26–A26.
- 73 Martin AR, Gignoux CR, Walters RK, Wojcik GL, Neale BM, Gravel S *et al.* Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. *Am J Hum Genet* 2017; **100**: 635–649.
- 74 Haro JM, Arbabzadeh-Bouchez S, Brugha TS, de Girolamo G, Guyer ME, Jin R *et al.* Concordance of the Composite International Diagnostic Interview Version 3.0 (CIDI 3.0) with standardized clinical assessments in the WHO World Mental Health surveys. *Int J Methods Psychiatr Res* 2006; **15**: 167–180.

- 75 Kessler RC, Wittchen H-U, Abelson JM, McGonagle K, Schwarz N, Kendler KS *et al.* Methodological studies of the Composite International Diagnostic Interview (CIDI) in the US national comorbidity survey (NCS). *Int J Methods Psychiatr Res* 1998; **7**: 33–55.
- 76 Nusslock R, Alloy LB. Reward processing and mood-related symptoms: An RDoC and translational neuroscience perspective. *J Affect Disord* 2017; **216**: 3–16.
- 77 Meehl PE. Schizotaxia, schizotypy, schizophrenia. *Am Psychol* 1962; **17**: 827–838.
- 78 Bleuler M. Conception of schizophrenia within the last fifty years and today [abridged]. *Proc R Soc Med* 1963; **56**: 945.
- 79 Rosenthal D. A suggested conceptual framework. In: Rosenthal D (ed). *The Genain quadruplets: A case study and theoretical analysis of heredity and environment in schizophrenia*, (pp. Basic Books, xiv: New York, NY, US, 1963, pp 505–511.
- 80 Nussey DH, Wilson AJ, Brommer JE. The evolutionary ecology of individual phenotypic plasticity in wild populations. *J Evol Biol* 2007; **20**: 831–844.
- 81 Fuemmeler BF, Dedert E, McClernon FJ, Beckham JC. Adverse childhood events are associated with obesity and disordered eating: results from a U.S. population-based survey of young adults. *J Trauma Stress* 2009; **22**: 329–333.
- 82 Metzler M, Merrick MT, Klevens J, Ports KA, Ford DC. Adverse childhood experiences and life opportunities: Shifting the narrative. *Child Youth Serv Rev* 2017; **72**: 141–149.
- 83 Jaffee SR, Ambler A, Merrick M, Goldman-Mellor S, Odgers CL, Fisher HL *et al.* Childhood Maltreatment Predicts Poor Economic and Educational Outcomes in the Transition to Adulthood. *Am J Public Health* 2018; **108**: 1142–1147.
- 84 Danese A, Tan M. Childhood maltreatment and obesity: systematic review and meta-analysis. *Mol Psychiatry* 2014; **19**: 544–554.
- 85 Cross-Disorder Group of the Psychiatric Genomics Consortium. Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. *Lancet* 2013; **381**: 1371.
- 86 Hill WD, Hagenaars SP, Marioni RE, Harris SE, Liewald DCM, Davies G *et al.* Molecular Genetic Contributions to Social Deprivation and Household Income in UK Biobank. *Curr Biol* 2016; **26**: 3083–3089.





